IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

GOJKOVIC, Zoran

Serial No.: 10/564,088

For: YELLOW FEVER MOSQUITO
DEOXYRIBONUCLEOSIDE
KINASE AND ITS USE

Art Unit: 1652

Washington, R.

April 29, 2008

Docket No.: GOJKOVIC=3

Confirmation No.: 7165

ELECTION WITH TRAVERSE

U.S. Patent and Trademark Office Customer Service Window Randolph Building 401 Dulany Street Alexandria, VA 22314

sir:

In response to the restriction requirement mailed March 31, 2008, please enter the following remarks.

1. In response to the group level restriction, applicants elect group 1 with traverse.

The Examiner argues that there is an <u>a posteriori</u> lack of unity in that the common technical feature linking the 8 groups is taught by Knecht, et al. (2003) and therefore fails to qualify as a "special" technical feature.

Knecht et al (2003) allegedly teaches a mosquito polynucleotide which encodes a polypeptide having 82% sequence identity to SEQ ID NO:2 according to a BlastP alignment.

A 39 page BLASTP search dated March 24, 2008 was attached to the office action. The action says that the Knecht et al. (2003) sequence is the "second alignment" on page 6. There is a partial sequence at the beginning of page 6, so we are not sure whether the Examiner is referring to the sequence XP_321524.1 or the second <u>full</u> sequence on that page, CAD 27756.1. Both sequences are reported to have a sequence identity <u>in the region of overlap</u> of 82%, consistent with the office action. <u>Neither</u> sequence is listed as <u>Aedes aegypti</u> as suggested by the action; rather, they are <u>Anopheles gambiae</u>.

The XP_321524.1 sequence is also listed as AA049462.1, and the NCBI database identifies that sequence as corresponding to the 246 a.a. sequence published in Knecht et al. (2003) (ref. AE) and submitted to GenBank on February 25, 2002. (Ex. A). Hence, we will assume that this is the intended sequence.

The aforementioned alignment is of amino acids "18-261" of the query sequence with amino acids 4-246 of the 246 a.a. subject sequence. Given that SEQ ID NO:2 is 248 a.a., we are not sure that the examiner used the correct query sequence, since the "18-261" doesn't make sense. Clarification is requested.

The percentage identity for the alignment is calculated by BlastP from 202 identities in a 244 a.a. overlap, i.e., as 82.79%. The examiner is respectfully reminded that at page 7, lines 2-7, the specification teaches that percentage identity is to be determined over the entire length of SEQ ID NO:2 (248 a.a.) and not merely over the region of overlap calculated by BlastP. Aligning the N-terminal of our SEQ ID NO:2 with AA044462 so our IGPER aligns with the database IASEK, we have

Query: MAAAIGPER Subjt: -MPPIASEK

i.e., no new identities (can't align the Met's without introducing a gap which would reduce the alignment score), and thus instead of 202 identities out of a 244 a.a. overlap (which includes one gap in the subject sequence), there are 202/248=81.45%.

In any event, taking at face value the action's assertion that a prior art sequence characterized by over 80% (if not 82%) identity exists, the holding of <u>a posteriori</u> lack of unity should be withdrawn because claim 1 has been amended to recite at least 85% identity.

3. Applicants have elected group 1, and hence the conditional species restrictions (for groups 3, 4, 5 and 6) are moot.

Thus, at least groups 1 claims 1-9, 16, 19, 20, 22 and 55

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must be examined.

Since the group restriction has been traversed, there is the possibility that groups 2-8 will be rejoined. If so, those species restrictions will be triggered. To expedite prosecution, applicants make the following species elections, all with traverse.

- a) adenoviral vector
- b) stem cells
- c) ara C
- d) ara C
- e) tumor cell
- f) ara C.

Restrictions a) and b) were conditional on group 3 and all group 3 claims read on elected species a) and b).

Restrictions c), d) and f) were conditional on groups 4, 5 and 6 respectively, and all groups 4-6 claims read on elected ara C.

Restrictions e) was conditional on group 6 (claims 38-40); of these claims, only claim 39 reads on a tumor cell.

4. The species restrictions are traversed on the ground that generic claims are allowable.

Respectfully submitted,

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